

#6 1/2

DATE: 07/27/2001
TIME: 20:00:12RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/807,007

ENTERED

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3 <110> APPLICANT: ZAPHIROPOULOS, Peter et al.
5 <120> TITLE OF INVENTION: A NOVEL COMPONENT IN THE HEDGEHOG SIGNALLING PATHWAY
7 <130> FILE REFERENCE: 2921-0130P
9 <140> CURRENT APPLICATION NUMBER: 09/807,007
10 <141> CURRENT FILING DATE: 2001-04-06
12 <160> NUMBER OF SEQ ID NOS: 16
14 <170> SOFTWARE: PatentIn version 3.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 1146
18 <212> TYPE: PRT
19 <213> ORGANISM: Homo sapiens
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31 Pro Leu Trp Leu Arg Ala Tyr Phe Gln Gly Leu Leu Phe Ser Leu Gly
32 35 40 45
35 Cys Gly Ile Gln Arg His Cys Gly Lys Val Leu Phe Leu Gly Leu Leu
36 50 55 60
39 Ala Phe Gly Ala Leu Ala Leu Gly Leu Arg Met Ala Ile Ile Glu Thr
40 65 70 75 80
43 Asn Leu Glu Gln Leu Trp Val Glu Val Gly Ser Arg Val Ser Gln Glu
44 85 90 95
47 Leu His Tyr Thr Lys Glu Lys Leu Gly Glu Glu Ala Ala Tyr Thr Ser
48 100 105 110
51 Gln Met Leu Ile Gln Thr Ala Arg Gln Glu Gly Glu Asn Ile Leu Thr
52 115 120 125
55 Pro Glu Ala Leu Gly Leu His Leu Gln Ala Ala Leu Thr Ala Ser Lys
56 130 135 140
59 Val Gln Val Ser Leu Tyr Gly Lys Ser Trp Asp Leu Asn Lys Ile Cys
60 145 150 155 160
63 Tyr Lys Ser Gly Val Pro Leu Ile Glu Asn Gly Met Ile Glu Arg Met
64 165 170 175
67 Ile Glu Lys Leu Phe Pro Cys Val Ile Leu Thr Pro Leu Asp Cys Phe
68 180 185 190
71 Trp Glu Gly Ala Lys Leu Gln Gly Gly Ser Ala Tyr Leu Pro Gly Arg
72 195 200 205
75 Pro Asp Ile Gln Trp Thr Asn Leu Asp Pro Glu Gln Leu Leu Glu Glu
76 210 215 220
79 Leu Gly Pro Phe Ala Ser Leu Glu Gly Phe Arg Glu Leu Leu Asp Lys
80 225 230 235 240
83 Ala Gln Val Gly Gln Ala Tyr Val Gly Arg Pro Cys Leu His Pro Asp
84 245 250 255
87 Asp Leu His Cys Pro Pro Ser Ala Pro Asn His His Ser Arg Gln Ala
88 260 265 270
91 Pro Asn Val Ala His Glu Leu Ser Gly Gly Cys His Gly Phe Ser His

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92          275          280          285
95 Lys Phe Met His Trp Gln Glu Glu Leu Leu Leu Gly Gly Met Ala Arg
96          290          295          300
99 Asp Pro Gln Gly Glu Leu Leu Arg Ala Glu Ala Leu Gln Ser Thr Phe
100 305          310          315          320
103 Leu Leu Met Ser Pro Arg Gln Leu Tyr Glu His Phe Arg Gly Asp Tyr
104          325          330          335
107 Gln Thr His Asp Ile Gly Trp Ser Glu Glu Gln Ala Ser Thr Val Leu
108          340          345          350
111 Gln Ala Trp Gln Arg Arg Phe Val Gln Leu Ala Gln Glu Ala Leu Pro
112          355          360          365
115 Glu Asn Ala Ser Gln Gln Ile His Ala Phe Ser Ser Thr Thr Leu Asp
116          370          375          380
119 Asp Ile Leu His Ala Phe Ser Glu Val Ser Ala Ala Arg Val Val Gly
120 385          390          395          400
123 Gly Tyr Leu Leu Met Leu Ala Tyr Ala Cys Val Thr Met Leu Arg Trp
124          405          410          415
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128          420          425          430
131 Val Ala Leu Ala Val Ala Ser Gly Leu Gly Leu Cys Ala Leu Leu Gly
132          435          440          445
135 Ile Thr Phe Asn Ala Ala Thr Thr Gln Val Leu Pro Phe Leu Ala Leu
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139 Gly Ile Gly Val Asp Asp Val Phe Leu Leu Ala His Ala Phe Thr Glu
140 465          470          475          480
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144          485          490          495
147 Arg Thr Gly Thr Ser Val Val Leu Thr Ser Ile Asn Asn Met Ala Ala
148          500          505          510
151 Phe Leu Met Ala Ala Leu Val Pro Ile Pro Ala Leu Arg Ala Phe Ser
152          515          520          525
155 Leu Gln Ala Ala Ile Val Val Gly Cys Thr Phe Val Ala Val Met Leu
156          530          535          540
159 Val Phe Pro Ala Ile Leu Ser Leu Asp Leu Arg Arg Arg His Cys Gln
160 545          550          555          560
163 Arg Leu Asp Val Leu Cys Cys Phe Ser Ser Pro Cys Ser Ala Gln Val
164          565          570          575
167 Ile Gln Ile Leu Pro Gln Glu Leu Gly Asp Gly Thr Val Pro Val Gly
168          580          585          590
171 Ile Ala His Leu Thr Ala Thr Val Gln Ala Phe Thr His Cys Glu Ala
172          595          600          605
175 Ser Ser Gln His Val Val Thr Ile Leu Pro Pro Gln Ala His Leu Val
176          610          615          620
179 Pro Pro Pro Ser Asp Pro Leu Gly Ser Glu Leu Phe Ser Pro Gly Gly
180 625          630          635          640
183 Ser Thr Arg Asp Leu Leu Gly Gln Glu Glu Glu Thr Arg Gln Lys Ala
184          645          650          655
187 Ala Cys Lys Ser Leu Pro Cys Ala Arg Trp Asn Leu Ala His Phe Ala
188          660          665          670

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191 Arg Tyr Gln Phe Ala Pro Leu Leu Leu Gln Ser His Ala Lys Ala Ile
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199 Thr Leu Val Gln Asp Gly Leu Ala Leu Thr Asp Val Val Pro Arg Gly
200 705                               710                               720
203 Thr Lys Glu His Ala Phe Leu Ser Ala Gln Leu Arg Tyr Phe Ser Leu
204                               725                               735
207 Tyr Glu Val Ala Leu Val Thr Gln Gly Gly Phe Asp Tyr Ala His Ser
208                               740                               750
211 Gln Arg Ala Leu Phe Asp Leu His Gln Arg Phe Ser Ser Leu Lys Ala
212                               755                               765
215 Val Leu Pro Pro Pro Ala Thr Gln Ala Pro Arg Thr Trp Leu His Tyr
216 770                               775                               780
219 Tyr Arg Asn Trp Leu Gln Gly Ile Gln Ala Ala Phe Asp Gln Asp Trp
220 785                               790                               800
223 Ala Ser Gly Arg Ile Thr Arg His Ser Tyr Arg Asn Gly Ser Glu Asp
224                               805                               815
227 Gly Ala Leu Ala Tyr Lys Leu Leu Ile Gln Thr Gly Asp Ala Gln Glu
228                               820                               830
231 Leu Leu Asp Phe Ser Gln Leu Thr Thr Arg Lys Leu Val Asp Arg Glu
232                               835                               845
235 Gly Leu Ile Pro Pro Glu Leu Phe Tyr Met Gly Leu Thr Val Trp Val
236 850                               855                               860
239 Ser Ser Asp Pro Leu Gly Leu Ala Ala Ser Gln Ala Asn Phe Tyr Pro
240 865                               870                               875
243 Pro Pro Pro Glu Trp Leu His Asp Lys Tyr Asp Thr Thr Gly Glu Asn
244                               885                               895
247 Phe Arg Ile Pro Pro Ala Gln Pro Leu Glu Phe Ala Gln Phe Pro Phe
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251 Leu Leu Arg Gly Leu Gln Lys Thr Ala Asp Phe Val Glu Ala Ile Glu
252 915                               920                               925
255 Gly Ala Arg Ala Ala Cys Ala Glu Ala Gly Gln Ala Gly Val His Ala
256 930                               935                               940
259 Tyr Pro Ser Gly Ser Pro Phe Leu Phe Trp Glu Gln Tyr Leu Gly Leu
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263 Arg Arg Cys Phe Leu Leu Ala Val Cys Ile Leu Leu Val Cys Thr Phe
264                               965                               975
267 Leu Val Cys Ala Leu Leu Leu Leu Asn Pro Trp Thr Ala Gly Leu Ile
268                               980                               990
271 Val Leu Val Leu Ala Met Met Thr Val Glu Leu Phe Gly Ile Met Gly
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280 1025                               1030                               1035
283 Gly Phe Leu Thr Thr Gln Gly Ser Arg Asn Leu Arg Ala Ala His
284 1040                               1045                               1050
287 Ala Leu Glu His Thr Phe Ala Pro Val Thr Asp Gly Ala Ile Ser

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288	1055	1060	1065
291	Thr Leu Leu Gly Leu Leu Met Leu Ala Gly Ser His Phe Asp Phe		
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295	Ile Val Arg Tyr Phe Phe Ala Ala Leu Thr Val Leu Thr Leu Leu		
296	1085	1090	1095
299	Gly Leu Leu His Gly Leu Val Leu Leu Pro Val Leu Leu Ser Ile		
300	1100	1105	1110
303	Leu Gly Pro Pro Pro Glu Val Ile Gln Met Tyr Lys Glu Ser Pro		
304	1115	1120	1125
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325	cgtgcttact tccagggcct gctcttctct ctgggatgcg ggatccagag acattgtggc	180	
327	aaagtgtctt ttctgggact gttggccttt ggggccctgg cattaggtct ccgcatggcc	240	
329	attattgaga caaacttgga acagctctgg gtagaagtgg gcagccgggt gagccaggag	300	
331	ctgcattaca ccaaggagaa gctgggggag gaggtgcat acacctctca gatgctgata	360	
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335	caggcagccc tcaactgccag taaagtccaa gtatcactct atgggaagtc ctgggatttg	480	
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389 gccccgttgc tgctccagtc acatgctaag gccatcgtgc tgggtgctctt tgggtgctctt 2100
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451 <210> SEQ ID NO: 4
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